Visualizing Differences of DTI Fiber Models

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Abstract—This paper…

Index Terms—DTI, fiber tracking, uncertainty, difference visualization.

INTRODUCTION

Diffusion Tensor Imaging (DTI) is a non-invasive technique to investigate the underlying anatomical structures. It measures the diffusion of water molecules in different directions. In pure water (e.g. the brain grey matter), isotropy is presented. In fibrous tissues (e.g. muscle, the brain white matter), anisotropy is shown. By fitting the diffusion profile with a Gaussian model, a 2nd-order tensor field is derived from the raw diffusion weighted imaging (DWI) volume. Then, a bunch of fibers are produced by tracking the trajectories of the fastest diffusion with line integral methods in the tensor field. This process is known as Fiber Tracking or Tractography, which has been demonstrated a useful tool to study connectivity information in a DTI dataset. It has been widely used in the research of cerebral ischemia, neurodegenerative diseases, and so on.

DTI fibers varies from subject to subject due to the variation in anatomy, and from scan to scan caused by subject positions, motions, and signal noise. In addition, DTI fibers are also sensitive to the tracking parameters and/or methods employed in tractography. Typical tracking parameters include the length threshold, the curvature threshold, the FA threshold, and so on. On the other hand, different algorithms for fiber tracking have been developed as well, either based on line propagation or energy minimization [cite]. Comparison among two or more DTI fiber models can help users identify the differences among them and understand the uncertainties in the DTI fiber models. Clinical applications of DTI fiber modes will be more likely after the doctors understand the sources of uncertainties and how these fiber models are affected by the uncertainties.

Characterizing, representing, and visualizing the differences within a collection of DTI fiber models is not a trivial task [cite].

1 RELATED WORK

2 OUR APPROACH

To enable comparison in a common coordinate system, all DTI datasets are first mapped into a normalized atlas space. In our implementation, DTI datasets from 50 normal participants are employed to create the DTI atlas. Any given DTI dataset will be registered with the average atlas tensor volume. In our implementation, the open-source registration tool DTI-Reg [cite] is adopted. The fiber model derived from the average atlas tensor volume is called the template fiber model which is the baseline to investigate differences. For simplicity, we denote the template fiber model as F_t.

In this paper, we concentrate on difference introduced by parameters and algorithms. Therefore, a fixed seeding strategy is used. Given a set of tracking configurations $\mathbf{C} = \{c_i | i = 1,2,\dots,n\}$, a fixed set of seeding points $\mathbf{S} = \{s_j | j = 1,2,\dots,m\}$, and the registered DTI datasets, we can obtain a set of fiber models $\mathbf{F} = \{F_i | i = 1,2,\dots,n\}$. $F_i = \{f_i^j | j = 1,2,\dots,m\}$ represents a fiber model. Generally, a fiber $f_i^j = \{p_k\}$ is represented as a set of consecutive points.

2.1 Structuring the Fiber Database

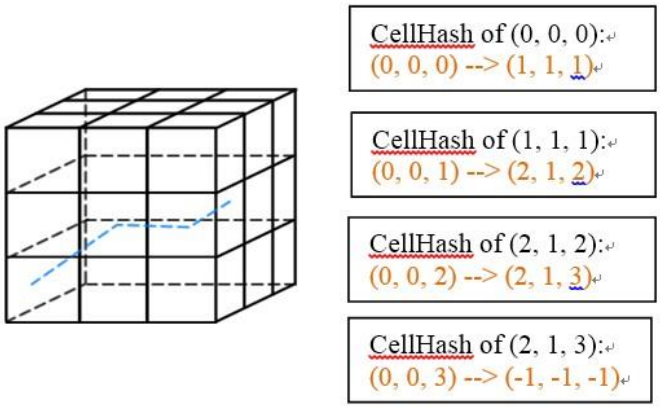


Figure 1 Illustration of the CellHash based fiber database.

To support fast random access of fibers in the 3D fiber space, we design a hash-based database to store all fiber models including the template fiber model F_t. More specifically, we discretize the entire 3D fiber space into cells with fixed width. The cell width is determined by the minimum distance between any two consecutive points in a fiber.

In each cell, we record two pieces of information: density and fibers passing the cell. The density of a cell indicates how often a cell is visited. If a fiber pass a cell, the density counter will be increased by 1.

All fibers passing a cell are recorded in a hash table called as **CellHash**. The key of a CellHash is a tuple (i, j, k), which implies that f_{ij} in F_i passes the cell at its k-th point. Accordingly, the value of a CellHash is also a tuple (x, y, z) that is the next cell the fiber f_{ij} will pass. The tuple (-1, -1, -1) represents the end of a fiber. Figure 1 shows the structures of the CellHash based fiber database.

In general, using CellHash to store fibers has the following properties:

- Fast random access.
- Streaming update.

2.2 Quantifying Differences

Generally, different tracking configurations have a great impact on the fiber length and/or shape. The following sections describes the methods to model difference in terms of fiber length and fiber shape.

Let $\xi_j = \{f_i^j | i = 1,2,\dots,n\}$ be a set of fibers produced by different tracking configuration at seeding point s_j and f_t^j be the template fiber at seeding point s_j. For convenience, we refer to $f_i^j \in \xi_j$ as target fiber.

2.2.1 Fiber Length

In statistics, the mean squared error (MSE) is a widely used measure to model the difference between values implied by estimators and the

true values. In spired by this principle, we define the length difference between the target fibers and the template fiber as a sum of the statistical variance and the statistical bias:

$$Diff_L(\xi_j, f_t^j) = \frac{\sum_{i=1}^{n}(L(f_i^j) - \bar{L}(\xi_i))^2}{n} + (\bar{L}(\xi_i) - L(f_t^j))^2$$

Here, $L(\cdot)$ is the fiber length function and $\bar{L}(\cdot)$ represents the mean fiber length function. $\sigma_L^2 = \sum_{i=1}^{n}(L(f_i^j) - \bar{L}(\xi_i))^2/n$ denotes the statistical length variance of ξ_j, and $\eta_L = (\bar{L}(\xi_i) - L(f_t^j))^2$ is the statistical length bias of ξ_j.

2.2.2 Fiber Shape

In spired by [cite], we propose to model the shape difference between fibers as the Geometric distance in a feature space associated with Riemanian metric.

Let $\beta: [0,1] \to \mathbb{R}^3$ be parameterized curve, representing a fiber. The set of all rotations for a fiber is given by $\mathbf{SO}(3) = \{\boldsymbol{O} \in \mathbb{R}^3 | \boldsymbol{O}^T\boldsymbol{O} = \boldsymbol{I}, det(\boldsymbol{O}) = +1\}$. The set of all re-parameterizations for a fiber is $\Gamma = \{\gamma: [0,1] \to [0,1] | \gamma(0) = 0, \gamma(1) = 1\}$. For any $\gamma \in \Gamma$, $(\beta, \gamma)(\tau) = \beta(\gamma(\tau))$ is a re-parameterization of $\beta(\tau)$. As $\|\beta_1 - \beta_2\| \neq \|(\beta_1, \gamma) - (\beta_2, \gamma)\|$ in general, simply using the standard $\mathbb{L}^2$ metric to model difference between a pair of fibers is unfaithful.

To overcome this issue, a fiber β is represented by a square-root velocity function (SRVF):

$$q(\tau) = \frac{\dot{\beta}(\tau)}{\sqrt{\|\dot{\beta}(\tau)\|}}, q: [0,1] \to \mathbb{R}^3$$

Where, $\dot{\beta}(\cdot)$ represents the velocity function. This representation is invariant to global translation. Using the SRVF representation, the shape difference between two fibers is defined as:

$$Diff_S(\beta_1, \beta_2) = \min_{\gamma \in \Gamma, \mathbf{O} \in \mathbf{SO}(3)} \cos^{-1}\left(\int_0^1 \langle (q_1, \gamma)(\tau), \mathbf{O}(q_2, \gamma)(\tau) \rangle d_\tau\right)$$

For further detail to solve this minimization problem, please refer to [cite].

$Diff_S(f_i^j, f_t^j)$ measures the shape difference between the target fiber f_i^j and the template fiber f_t^j. Further, the average shape difference $\mu_S = \sum_{i=1}^{n} Diff_S(f_i^j, f_t^j)/n$ quantifies the difference between the given target fibers to the template fiber. Larger μ_S means the given target fibers are much more different from the template fiber. The variance of the shape differences $\sigma_S^2 = \sum_{i=1}^{n}(Diff_S(f_i^j, f_t^j) - \mu_S)^2/n$ quantifies the similarities among the target fibers. Larger σ_S^2 indicates that the tareget fibers are quite dissimilar to each other.

2.3 Visualizing Differences

As described in Section 2.2, we know that η_L and μ_S quantify the difference between the target fibers to the template fiber. σ_L^2 and σ_S^2 quantify the difference among target fibers. Enlightened by these observations, we choose to use a quadrant scatterplot to characterize and visualize different types of difference. Specifically, the horizontal axis of the quadrant scatterplot represents the difference between the target fibers to the template fibers. The vertical axis of the quadrant scatterplot represents the difference among the target fibers. Each axis is associated with a threshold.

2.3.1 The Fiber Length Quadrant Scatterplot

Figure 2 shows different types of difference in terms of fiber length. For illustration, exemplar 2D fibers are displayed in each quadrant. Points in different quadrants are encoded with different colors. This simple scheme allows users easily review the types of difference in different regions (see Figure 3).

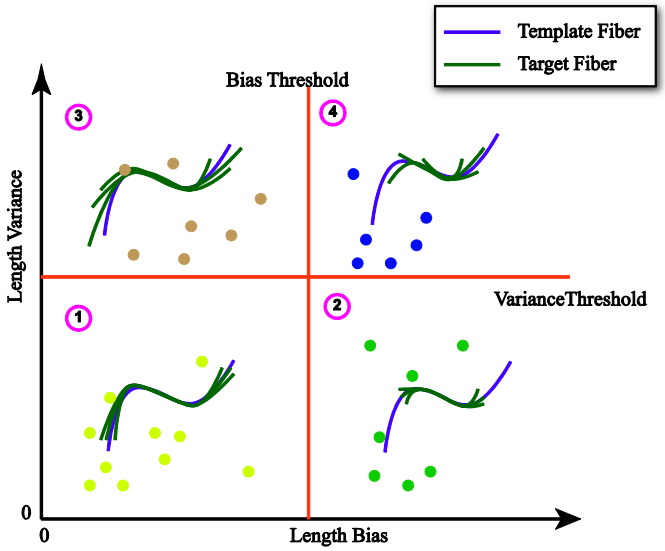


Figure 2 This figure shows four different types between the target fibers to the template fiber in terms of fiber length.

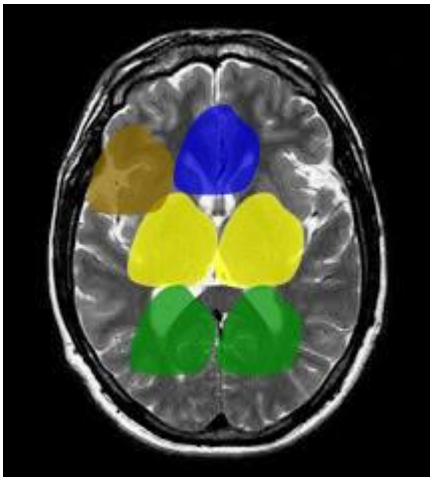
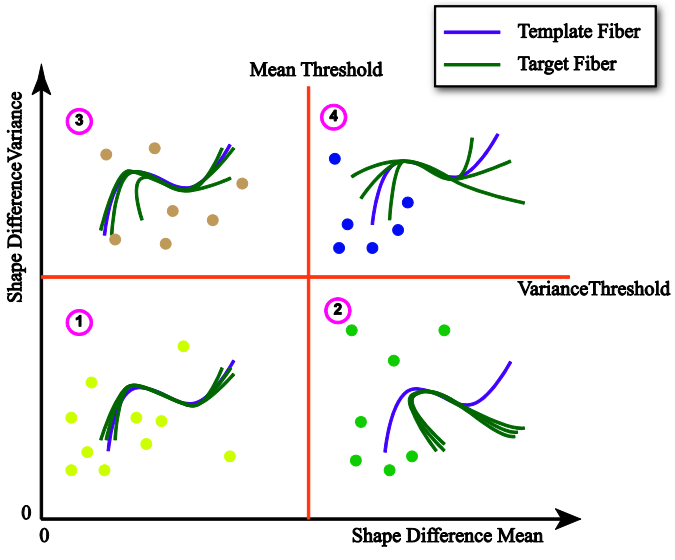


Figure 3 Difference visualization in the DTI volum.

2.3.2 The Fiber Shape Quadrant Scatterplot



3 Results and Discussion

4 Evaluation

References

[1]